Amendments to the Specification

Please amend the paragraph beginning at page 4, line 16, as follows:

According to yet another aspect of the invention, there is provided a computer-readable medium having recorded thereon x-ray crystallographic coordinate data for the catalytic domain of TNF-α converting enzyme, or a portion thereof. In one embodiment, the computer-readable medium has recorded thereon the x-ray crystallographic coordinate data set forth in Table 1 (SEQ ID NO:11), or a portion thereof. In another embodiment, the medium is selected from the group consisting of a floppy disc, a hard disc, computer tape, RAM, ROM, CD, DVD, a magnetic disk, and an optical disk. In still another embodiment, the computer-readable medium has recorded thereon machine-readable data, wherein the computer-readable medium, when used in conjunction with a machine programmed with instructions for using the data, is capable of generating image signals for depicting a graphical, three-dimensional representation of a TNF-α converting enzyme polypeptide, or portion thereof.

Please amend the paragraph beginning at page 22, line 4, as follows:

The C-terminal chain comprising the last 61 TCD residues (Fig. 3) first forms three short straight almost perpendicularly arranged segments linked by two "narrow" supertwisted loops, returns via the tight "Met-turn" Tyr433-Val434-Met435-Tyr436 (SEQ ID NO:10) back to the surface where it kinks at Pro437 to form the Pro437-Ile438-Ala439 outer "wall" of the S1' crevice, approaches in a wide loop the C-terminal α-helix hD and runs through it, and ends up on the molecular "back" surface close to the N-terminus, with the last defined residues Arg473-Ser474 fixed via hydrogen bonds to the main molecular body. Via Cys423-Cys453, the first of the two "narrow" loops is disulfide-linked with the N-terminus of helix hD, whose C-terminal end in turn is clamped to the "ear-like" sIV-sV linker peptide through Cys365-Cys469. Spatially adjacent, the third disulfide bridge of TCD, Cys225-Cys333, connects the N-terminal parts of β-strands sI and sIII. In the intact TACE molecule, four residues downstream of Ser474 would reside Cys478, which is already integral part of the compact elongated disintegrin domain (Saudek *et al.*, "Three-dimensional structure of echistatin, the smallest active RGD protein" *Biochem.* 30, 7369-7372 (1991)). Considering Ser474 and this Cys478 as pivot points of their respective domains, the three residue linker would allow relatively unconstrained docking of the disintegrin domain to the "left" surface side of the catalytic domain.